SEQUENCE LISTING

- (1) GENERAL INFORMATION
 - (i) APPLICANT:
 Seidel, Christoph; Weinhues, Ursula-Henrike;
 Schmitt, Urban; Motz, Manfred; Wiedmann, Michael;
 Upmeier, Barbara; Soutscheck, Erwin
 - (ii) TITLE OF INVENTION:

 Recombinant antigen from the NS3 region of the hepatitis C virus
 - (iii) NUMBER OF SEQUENCES: 9
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Felfe & Lynch
 - (B) STREET: 805 Third Avenue
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: USA
 - (F) ZIP: 10022
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
 - (B) COMPUTER: IBM PS/2
 - (C) OPERATING SYSTEM: PC-DOS
 - (D) SOFTWARE: PatentIn Relase #1.0, Version #1.25 (EPA)
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/511,759
 - (B) FILING DATE: 7-AUGUST-1995y
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: p 44 28 705.4
 - (B) FILING DATE: 12 AUGUST 1994
 - (viii) ATTORNEY/AGENT INFORMATION
 - (A) NAME: HANSON, NORMAN
 - (B) REGISTRATION NUMBER: 30, 946
 - (C) REFERENCE/DOCKET NUMBER: HUBR 1067.1
 - (ix) TELECOMMUNICATION INFORMATION
 - (A) TELEPHONE: 212-688-9200
 - (B) TELEFAX: 212-838-3884

INFORMATION FOR SEQ ID NO: (2) SEQUENCE CHARACTERISTICS: (i) LENGTH: 885 base pairs (A) TYPE: nucleic acid (B) STRANDEDNESS: both (C) linear TOPOLOGY: (D) (ii) MOLECULE TYPE: cDNA (vi) INITIAL ORIGIN: (A) ORGANISM: hepatitis C virus (viii) POSITION IN GENOME: CHROMOSOME SEGMENT: (A) (ix) CHARACTERISTICS: (A) NAME/KEY: CDS LOCATION: 1..885 (B) (xi) SEQUENCE DESCRIPTION: SEO ID NO: 1: ATG ACC ATG ATT ACG AAT TCC CGG GGA TCC ATC ATG AAA TCC CCG GTG 48 Met Thr Met Ile Thr Asn Ser Arg Gly Ser Ile Met Lys Ser Pro Val TTC ACG GAT AAC TCC TCT CCA CCG GTA GTG CCC CAG AGC TTC CAG GTG 96 Phe Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val 20 GCT CAC CTG CAT GCT CCC ACA GGC AGC GGC AAG AGC ACC AAG GTC CCG 144 Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro GCT GCA TAC GCA GCT CAG GGC TAC AAG GTG CTA GTG CTC AAC CCT TCT 192 Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser 50 GTT GCT GCA ACA TTG GGC TTT GGT GCC TAC ATG TCC AAG GCT CAT GGG 240 Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly 80 65 ATC GAT CCT AAC ATC AGG ACC GGG GTG AGA ACA ATT ACC ACT GGC AGC 288 Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser 90 CCC ATT ACG TAC TCC ACT TAC GGC AAG TTT CTT GCC GAC GGC GGG TGC 336 Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys 105 100

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|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|---|-----|--|
| | GGG Gly | | | | | | | | | | | | | | | • | 384 | |
| | GCC Ala 130 | Thr | | | | | | | | | | | | | | | 432 | |
| | GCG Ala | | | | | | | | | | | | | | | | 480 | |
| | GTC Val | | | | | | | | | | | | | | | | 528 | |
| | GGA Gly | | | | | | | | | | | | | | | | 576 | |
| AAG Iys I | GGG Gly | | | | | | | | | | | | | | | | 624 | |
| GAG GGlu | | | | | | | | | | | | | | | | | 672 | |
| TAC Tyr 225 | Arq | GGT Gly | CTT Leu | GAC Asp | GTG Val 230 | TCC Ser | GTC Val | ATC Ile | CCG Pro | ACC Thr 235 | AGC Ser | GGT Gly | GAT Asp | GTT Val | GTC Val 240 | | 720 | |
| GTC Val | GTG Val | GCA Ala | ACC Thr | GAC Asp 245 | GCC Ala | CTC Leu | ATG Met | ACC Thr | GGC Gly 250 | TAT Tyr | ACC Thr | GGC Gly | GAC Asp | TTC Phe 255 | GAC Asp | | 768 | |
| TCG Ser | GTG Val | ATA Ile | GAC Asp 260 | TGC Cys | AAC Asn | ACG Thr | TGT Cys | GTC Val 265 | ACT Thr | CAG Gln | ACA Thr | GTC Val | GAT Asp 270 | TTC Phe | AGC Ser | | 816 | |
| CTT Leu | GAC Asp | CCT Pro 275 | ACC Thr | TTC Phe | ACC Thr | ATT Ile | GAG Glu 280 | ACG Thr | ACC Thr | ACA Thr | CTT Leu | CCC Pro 285 | CAG Gln | GAT Asp | GCT Ala | | 864 | |
| | TCC Ser 290 | | | | | | | | | | | | | | | | 885 | |
| | | | | . : | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | |

(3) <u>INFORMATION FOR SEQ ID NO:</u> 2

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Thr Met Ile Thr Asn Ser Arg Gly Ser Ile Met Lys Ser Pro Val 10

Phe Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val 20

Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro 35

Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser

Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly

65 70 75 80

Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser

85
90
95

Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys

Thala Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr

120 125

Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Gly Glu 130 135 140

Thr Ala Gly Ala Lys Leu Val Val Phe Ala Thr Ala Thr Pro Pro Gly
145 150 155 160-

Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr 165 170 175

Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile 180 185 190

Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Arg Lys Cys Asp 195 200 205

| Glu | Leu 210 | Ala | Thr | Lys | Leu | Val 215 | Ala | Met | Gly | Ile | Asn 220 | Ala | Val | Ala | Tyr |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Tyr 225 | Arg | Gly | Leu | Asp | Val 230 | Ser | Val | Ile | Pro | Thr 235 | Ser | Gly | Asp | Val | Val 240 |
| Val | Val | Ala | Thr | Asp 245 | Ala | Leu | Met | Thr | Gly 250 | Tyr | Thr | Gly | Asp | Phe 255 | Asp |
| Ser | Val | Ile | Asp 260 | Cys | Asn | Thr | Cys | Val 265 | Thr | Gln | Thr | Val | Asp 270 | Phe | Ser |
| Leu | Asp | Pro 275 | Thr | Phe | Thr | Ile | Glu 280 | Thr | Thr | Thr | Leu | Pro 285 | Gln | Asp | Ala |
| Val | Ser 290 | Arg | Thr | Gln | Arg | Arg 295 | | | | | | | | | |

3:

- (4) <u>INFORMATION FOR SEQ ID NO</u>:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AAGGGATCCA TCATGAAATC CCCGGTGTTC ACGGATAACT

(5) <u>INFORMATION FOR SEQ ID NO:</u> 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGGAAGCCTT AATTCTTACC GTCGTTGAGT GCGGGAGAC

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| (6) | INFORMATION FOR SEO ID NO: 5: | | |
|------------|--|---|----|
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | | |
| | (ii) MOLECULE TYPE: cDNA | · | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5: | | |
| GAGG | GGATCCA TCATGAAAGC GGTGGACTTT ATCCCTGTG | | 39 |
| (7) | INFORMATION FOR SEQ ID NO: 6: | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | | |
| | (ii) MOLECULE TYPE: cDNA | | |
| T. | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6: | | |
| J GAGA | AAGCTTT TAACACGTGT TGCAGTCTAT CAC | | 33 |
| [(8) [| INFORMATION FOR SEQ ID NO: 7: | | |
| | (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | | |
| | (ii) MOLECULE TYPE: cDNA | | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: | | |
| GAGG | GGATCCA TCATGAAACA CCTGCATGCT CCCACCGGC | | 39 |

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(8) INFORMATION FOR SEQ ID NO:

- (i) SEQUENCE CHARACTERISTICS:
 - LENGTH: 33 base pairs (A)
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GAGAAGCTTT TAATACCAAG CACAGCCTGC GTC

- (3) INFORMATION FOR SEQ ID NO:
 - (i) SEQUENCE CHARACTERISTICS:
 - LENGTH: 302 amino acids (A)
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION:

□Pro Val Glu Asn Leu Glu Thr Thr Met Arg Ser Pro Val Phe Thr □ 1 5 10 15

🕮 Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val Ala

His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro

Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro

Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala

His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr

Thr Gly Ser Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala 95 100

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|----------------|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|
| Asp | Gly | Gly | Cys | Ala 110 | Gly | Gly | Ala | Tyr | Asp 115 | Ile | Ile | Ile | Cys | Asp 120 |
| Glu | Cys | His | Ser | Thr 125 | Asp | Ala | Thr | Ser | Ile 130 | Leu | Gly | Ile | Gly | Thr 135 |
| Val | Leu | Asp | Gln | Gly 140 | Glu | Thr | Ala | Gly | Ala 145 | Lys | Leu | Val | Val | Phe 150 |
| Ala | Thr | Ala | Thr | Pro 155 | Pro | Gly | Ser | Val | Thr 160 | Val | Pro | His | Pro | Asn 165 |
| Ile | Glu | Glu | Val | Ala 170 | Leu | Ser | Thr | Thr | Gly 175 | Glu | Ile | Pro | Phe | Tyr 180 |
| Gly | Lys | Ala | Ile | Pro 185 | Leu | Glu | Val | Ile | Lys 190 | Gly | Gly | Arg | His | Leu 195 |
| Ile | Phe | Cys | His | Ser 200 | Lys | Arg | Lys | Cys | Asp 205 | Glu | Leu | Ala | Thr | Lys 210 |
| | Val | Ala | Met | Gly 215 | Ile | Asn | Ala | Val | Ala 220 | Tyr | Tyr | Arg | Gly | Leu 225 |
| 型 Masp 型 | Val | Ser | Val | Ile 230 | Pro | Thr | Ser | Gly | Asp 235 | Val | Val | Val | Val | Ala 240 |
| o Thr | | | | 245 | | | | | 250 | | | | | 255 |
| lle O | Asp | Cys | Asn | Thr 260 | Cys | Val | Thr | Gln | Thr 265 | Val | Asp | Phe | Ser | Leu 270 |
| Map Map | Pro | Thr | Phe | Thr 275 | Ile | Glu | Thr | Thr | Thr 280 | Leu | Pro | Gln | Asp | Ala 285 |
| | Ser | Arg | Thr | Gln 290 | Arg | Arg | Gly | Arg | Thr 295 | Gly | Arg | Gly | Lys | Pro 300 |
| Gly | Ile | | | | | | | | | | | | | |

Gly Ile 302

SEQUENCE PROTOCOL

- (1) GENERAL INFORMATION:
 - (i) APPLICANT:
 - (A) NAME: Boehringer Mannheim GmbH
 - (B) ROAD: Sandhofer Str. 112-132
 - (C) CITY: Mannheim
 - (E) COUNTRY: Germany
 - (F) POSTAL CODE: 68305
 - (ii) TITLE OF APPLICATION: Recombinant antigen from the NS3 region of the hepatitis C virus
 - (iii) NUMBER OF SEQUENCES: 8
 - (iv) COMPUTER READABLE FORM:
 - (A) DATA CARRIER: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 885 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRAND FORM: both
 - (D) TOPOLOGY: linear
 - (ii) TYPE OF MOLECULE: cDNA

(vi) INITIAL ORIGIN:

(A) ORGANISM: hepatitis C virus

(viii) POSITION IN THE GENOME:

(A) CHROMOSOME/SEGMENT: NS3

(ix) CHARACTERISTICS:

(A) NAME/KEY: CDS

(B) LOCATION: 1..885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

| ATG Met U 1 | Thr | ATG Met | ATT | ACG Thr 5 | AAT Asn | TCC | CGG Arg | GGA Gly | TCC Ser 10 | ATC Ile | ATG Met | AAA Lys | TCC | CCG Pro 15 | | 48 |
|-------------------|-------------------|-------------------|-------------------|-----------------|------------------|-------------------|-------------------|-------------------|------------------|------------------|-------------------|-------------------|-------------------|------------------|------------------|-----|
| TTC | ACG Thr | GAT Asp | AAC Asn 20 | Ser | TCT Ser | CCA Pro | CCG Pro | GTA Val 25 | GTG Val | CCC Pro | CAG Gln | AGC Ser | TTC Phe 30 | CAG Gln | GTG Val | 96 |
| GCT Ma | CAC His | CTG Leu 35 | CAT His | GCT Ala | CCC Pro | ACA Thr | GGC Gly 40 | AGC Ser | GGC Gly | AAG Lys | AGC Ser | ACC Thr 45 | AAG Lys | GTC Val | CCG Pro | 144 |
| SCT Ala | GCA Ala 50 | TAC Tyr | GCA Ala | GCT Ala | CAG Gln | GGC Gly 55 | TAC Tyr | AAG Lys | GTG Val | CTA Leu | GTG Val 60 | CTC Leu | AAC Asn | CCT Pro | TCT Ser | 192 |
| GTT Val 65 | GCT Ala | GCA Ala | ACA Thr | TTG Leu | GGC Gly 70 | TTT Phe | GGT Gly | GCC Ala | TAC Tyr | ATG Met 75 | TCC | AAG Lys | GCT Ala | CAT His | GGG Gly 80 | 240 |
| ATC | GAT | CCT | AAC | ATC | AGG | ACC | GGG | GTG | AGA | ACA | ATT | ACC | ACT | GGC | AGC | 288 |
| Ile | Asp | Pro | Asn | Ile 85 | Arg | Thr | Gly | Val | Arg 90 | Thr | Ile | Thr | Thr | Gly 95 | Ser | |
| CCC Pro | ATT Ile | ACG Thr | TAC Tyr 100 | TCC Ser | ACT Thr | TAC Tyr | GGC Gly | AAG Lys 105 | TTT Phe | CTT Leu | GCC Ala | GAC Asp | GGC Gly 110 | GGG Gly | TGC Cys | 336 |
| GCA Ala | GGG Gly | GGT Gly 115 | GCT Ala | TAT Tyr | GAC Asp | ATA Ile | ATA Ile 120 | ATT Ile | TGT Cys | GAC Asp | GAG Glu | TGC Cys 125 | CAC His | TCC Ser | ACG Thr | 384 |
| GAT Asp | GCC Ala 130 | ACA Thr | TCC Ser | ATC' Ile | TTG Leu | GGC Gly 135 | ATC Ile | GGC Gly | ACT Thr | GTC Val | CTT Leu 140 | GAC Asp | CAA Gln | GGA Gly | GAG Glu | 432 |

| ÁCT Thr 145 | GCG Ala | GGG Gly | GCG Ala | AAA Lys | Leu 150 | GTT Val | GTG Val | TTC Phe | GCC Ala | ACC Thr 155 | GCC Ala | cc Thr | CCT Pro | CCG Pro | GGC Gly 160 | 480 |
|-------------------|-------------------|------------|-------------------|-------------------|------------|-------------------|------------|-------------------|-------------------|-------------------|------------|------------|-------------------|-------------------|-------------------|-----|
| TCC Ser | GTC Val | ACT Thr | GTG Val | CCC Pro 165 | CAT His | ccc Pro | AAC Asn | ATT Ile | GAG Glu 170 | GAG Glu | GTT Val | GCT Ala | CTA Leu | TCC Ser 175 | ACC Thr | 528 |
| | | | | | | TAC Tyr | | | | | | | | | | 576 |
| | | | | | | ATC Ile | | | | | | | | | | 624 |
| | | | | | | GTC Val 215 | | | | | | | | | | 672 |
| | | | | | | TCC Ser | | | | | | | | | | 720 |
| GTC Val ∰ | GTG Val | GCA Ala | ACC Thr | GAC Asp 245 | GCC Ala | CTC Leu | ATG Met | ACC Thr | GGC Gly 250 | TAT Tyr | ACC Thr | GGC Gly | GAC Asp | TTC Phe 255 | GAC Asp | 768 |
| TCG Ser O | GTG Val | ATA Ile | GAC Asp 260 | TGC Cys | AAC Asn | ACG Thr | TGT Cys | GTC Val 265 | ACT Thr | CAG Gln | ACA Thr | GTC Val | GAT Asp 270 | TTC Phe | AGC Ser | 816 |
| | | | | | | ATT | | | | | | | | | | 864 |
| GTC Val | TCC Ser 290 | CGC Arg | ACT Thr | CAA Gln | CGA Arg | CGG Arg 295 | | | | | | | | | | 885 |

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

/207

Met Thr Met Ile Thr Asn Ser Arg Gly Ser Ile Met Lys Ser Pro Val

10 1 Phe Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro 35 Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ala Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Gly Glu 130 Thr Ala Gly Ala Lys Leu Val Val Phe Ala Thr Ala Thr Pro Pro Gly 155 Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr 170 Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Arg Lys Cys Asp 200 Glu Leu Ala Thr Lys Leu Val Ala Met Gly Ile Asn Ala Val Ala Tyr 210 215 Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Leu Pro Gln Asp Ala 280 285 1488 Val Ser Arg Thr Gln Arg Arg 295

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|---|----|
| (2) INFORMATION FOR SEQ ID NO: 3: | |
| (i) SEQUENCE CHARACTERISTICS: | |
| (A) LENGTH: 40 base pairs | |
| (B) TYPE: nucleic acid | |
| (C) STRAND FORM: single | |
| (D) TOPOLOGY: linear | |
| (ii) TYPE OF MOLECULE: cDNA | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: | |
| | |
| AAGGGATCCA TCATGAAATC CCCGGTGTTC ACGGATAACT | 40 |
| (2) INFORMATION FOR SEQ ID NO: 4: | |
| (i) SEQUENCE CHARACTERISTICS: | |
| (A) LENGTH: 39 base pairs | |
| (B) TYPE: nucleic acid | |
| (C) STRAND FORM: single | |
| (D) TOPOLOGY: linear | |
| (ii) TYPE OF MOLECULE: cDNA | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 | |
| GGGAAGCCTT AATTCTTACC GTCGTTGAGT GCGGGAGAC | 39 |
| (2) INFORMATION FOR SEQ ID NO: 5: | , |
| (i) SEQUENCE CHARACTERISTICS: | |
| (A) LENGTH: 39 base pairs | |
| (B) TYPE: nucleic acid | |
| (C) STRAND FORM: singl | |

| (D) TOPOLOGY: linear | |
|--|----|
| (ii) TYPE OF MOLECULE: cDNA | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 | |
| GAGGGATCCA TCATGAAAGC GGTGGACTTT ATCCCTGTG | 39 |
| (2) INFORMATION FOR SEQ ID NO: 6: | |
| (i) SEQUENCE CHARACTERISTICS: | v |
| (A) LENGTH: 33 base pairs | |
| (B) TYPE: nucleic acid | |
| (C) STRAND FORM: single | |
| (D) TOPOLOGY: linear | |
| (ii) TYPE OF MOLECULE: cDNA | · |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6 | |
| GAGAAGCTTT TAACACGTGT TGCAGTCTAT CAC | 33 |
| (2) INFORMATION FOR SEQ ID NO: 7: | |
| (i) SEQUENCE CHARACTERISTICS: | |
| (A) LENGTH: 39 base pairs | |
| (B) TYPE: nucleic acid | |
| (C) STRAND FORM: single | |
| (D) TOPOLOGY: linear | |

(ii) TYPE OF MOLECULE: cDNA

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: | |
|--|----|
| GAGGGATCCA TCATGAAACA CCTGCATGCT CCCACCGGC | 39 |
| (2) INFORMATION FOR SEQ ID NO: 8: | |
| (i) SEQUENCE CHARACTERISTICS: | |
| (A) LENGTH: 33 base pairs | |
| (B) TYPE: nucleic acid | |
| (C) STRAND FORM: single | |
| (D) TOPOLOGY: linear | |
| (ii) TYPE OF MOLECULE: cDNA | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8 | |
| GAGAAGCTTT TAATACCAAG CACAGCCTGC GTC | 33 |